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SEQUENCE LISTING

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WATAHIKI, Masanori

<120> RNA Polymerase

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<140> US 09/254,344

<141> 1999-09-03

<150> PCT/JP98/03037

<151> 1998-07-06

<150> JP 9/180883

<151> 1997-07-07

<150> JP 10/155759

<151> 1998-06-04

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<170> PatentIn version 3.0

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Pro	Ser	Glu	Thr	Val	Gln	Asp	Ile	Tyr	Gly	Ile	Val	Ala	Gln	Lys	Val
545					550					555					560
Asn	Glu	Ile	Leu	Lys	Gln	Asn	Gly	Thr	Pro	Asn	Glu	Met	Ile	Thr	Val
			565						570					575	
Thr	Asp	Lys	Asp	Thr	Gly	Glu	Ile	Ser	Glu	Lys	Leu	Lys	Leu	Gly	Thr
			580					585					590		

Fig 8 by ~

Ser Thr Leu (Ala Gln Gln Trp Leu Ala Tyr Gly Val Thr Arg Ser Val
 595 600 605
 Thr Lys Arg Ser Val (Met Thr Leu Ala Tyr Gly Ser Lys) Glu (Phe Gly
 610 615 620
 Phe Arg Gln Gln Val Leu Asp Asp Thr Ile Gln Pro Ala Ile Asp Ser
 625 630 635 640
 Gly Lys Phe Thr Gln Pro Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu
 645 650 655
 Ile Trp Asp Ala Val Ser Val Thr Val Val Ala Ala Val Glu Ala Met
 660 665 670
 Asn Trp Leu Lys Ser Ala Ala Lys Leu Leu Ala Ala Glu Val Lys Asp
 675 680 685
 Lys Lys Thr Lys Glu Ile Leu Arg His Arg Cys Ala Val His Trp Thr
 690 695 700
 Thr Pro Asp Gly Phe Pro Val Trp Gln Glu Pro Leu Gln Lys Arg Leu
 705 710 715 720
 Asp Met Ile Phe Leu Gly Gln Phe Arg Leu Gln Pro Thr Ile Asn Thr
 725 730 735
 Leu Lys Asp Ser Gly Ile Asp Ala His Lys Gln Glu Ser Gly Ile Ala
 740 745 750
 Pro Asn Phe Val His Ser Gln Asp Gly Ser Arg Leu Met Thr Val Val
 755 760 765
 Tyr Ala His Glu Lys Tyr Gly Ile Glu Ser Phe Ala Leu Ile His Asp
 770 775 780
 Ser Phe Gly Thr Ile Pro Gly Lys Leu Phe Lys Ala Val Arg Glu Thr
 785 790 795 800
 Met Val Ile Thr Tyr Glu Asn Asn Asp Val Leu Ala Asp Phe Tyr Ser
 805 810 815
 Gln Phe Ala Asp Gln Leu His Glu Thr Gln Leu Asp Lys Met Pro Pro
 820 825 830
 Leu Pro Lys Lys Gly Asn Leu Asn Leu Gln Asp Ile Leu Lys Ser Asp
 835 840 845
 Phe Ala Phe Ala
 850

<210> 5
 <211> 876
 <212> PRT
 <213> Bacteriophage K11

<400> 5
 Met Asn Ala Leu Asn Ile Gly Arg Asn Asp Phe Ser Glu Ile Glu Leu

1	5	10	15
Ala Ala Ile Pro Tyr Asn Ile Leu Ser Glu His Tyr Gly Asp Gln Ala	20	25	30
Ala Arg Glu Gln Leu Ala Leu Glu His Glu Ala Tyr Glu Leu Gly Arg	35	40	45
Gln Arg Phe Leu Lys Met Leu Glu Arg Gln Val Lys Ala Gly Glu Phe	50	55	60
Ala Asp Asn Ala Ala Ala Lys Pro Leu Val Leu Thr Gln Leu Thr Lys	65	70	75
Arg Ile Asp Asp Trp Lys Glu Glu Gln Ala Asn Ala Arg Gly Lys Lys	85	90	95
Pro Arg Ala Tyr Tyr Pro Ile Lys His Gly Val Ala Ser Glu Leu Ala	100	105	110
Val Ser Met Gly Ala Glu Val Leu Lys Glu Lys Arg Gly Val Ser Ser	115	120	125
Glu Ala Ile Ala Leu Leu Thr Ile Lys Val Val Leu Gly Asn Ala His	130	135	140
Arg Pro Leu Lys Gly His Asn Pro Ala Gln Leu Gly Lys Ala Leu Glu	145	150	155
Asp Glu Ala Arg Phe Gly Arg Ile Arg Glu Gln Glu Ala Ala Tyr Phe	165	170	175
Lys Lys Asn Val Ala Asp Gln Leu Asp Lys Arg Val Gly His Val Tyr	180	185	190
Lys Lys Ala Phe Met Gln Val Val Glu Ala Asp Met Ile Ser Lys Gly	195	200	205
Met Leu Gly Gly Asp Asn Trp Ala Ser Trp Lys Thr Asp Glu Gln Met	210	215	220
His Val Gly Thr Lys Leu Leu Ile Glu Gly Thr Gly Leu Val Glu Met	225	230	235
Thr Lys Asn Lys Met Ala Asp Gly Ser Asp Asp Val Thr Ser Met Gln	245	250	255
Met Val Gln Leu Ala Pro Ala Phe Val Glu Leu Leu Ser Lys Arg Ala	260	265	270
Gly Ala Leu Ala Gly Ile Ser Pro Met His Gln Pro Cys Val Val Pro	275	280	285
Pro Lys Pro Trp Val Glu Thr Val Gly Gly Gly Tyr Trp Ser Val Gly	290	295	300
Leu Ala Leu Val Arg Thr His Ser Lys Lys Ala Leu Arg Arg Tyr Ala	305	310	315
			320

Asp Val His Met Pro Glu Val Tyr Lys Ala Val Asn Leu Ala Gln Asn
 325 330 335
 Thr Pro Trp Lys Val Asn Lys Lys Val Leu Ala Val Val Asn Glu Ile
 340 345 350
 Val Asn Trp Lys His Cys Pro Val Gly Asp Val Pro Ala Ile Glu Arg
 355 360 365
 Glu Glu Leu Pro Pro Arg Pro Asp Asp Ile Asp Thr Asn Glu Val Ala
 370 375 380
 Arg Lys Ala Trp Arg Lys Glu Ala Ala Ala Val Tyr Arg Lys Asp Lys
 385 390 395 400
 Ala Arg Gln Ser Arg Arg Cys Arg Cys Glu Phe Met Val Ala Gln Ala
 405 410 415
 Asn Lys Phe Ala Asn His Lys Ala Ile Trp Phe Pro Tyr Asn Met Asp
 420 425 430
 Trp Arg Gly Arg Val Tyr Ala Val Ser Met Phe Gly Asn Asp Met Thr
 435 440 445
 Lys Gly Ser Leu Thr Leu Ala Lys Gly Lys Pro Ile Gly Leu Asp Gly
 450 455 460
 Phe Tyr Trp Leu Lys Ile His Gly Ala Asn Cys Ala Gly Val Asp Lys
 465 470 475 480
 Val Pro Phe Pro Glu Arg Ile Lys Phe Ile Glu Glu Asn Glu Gly Asn
 485 490 495
 Ile Leu Ala Ser Ala Ala Asp Pro Leu Asn Thr Trp Trp Thr Gln Gln
 500 505 510
 Asp Ser Pro Phe Ala Phe Cys Phe Glu Tyr Ala Gly Val Lys His His
 515 520 525
 Gly Leu Asn Ser Tyr Asn Cys Ser Leu Pro Leu Ala Phe Asp Gly Ser
 530 535 540
 Cys Ser Gly Ile Gln His Phe Ser Ala Met Leu Arg Asp Glu Val Gly
 545 550 555 560
 Gly Arg Ala Val Asn Leu Leu Pro Ser Asp Thr Val Asp Ile Tyr Lys
 565 570 575
 Ile Val Ala Asp Lys Val Asn Glu Val Leu His Gln Asn Gly Ser Gln
 580 585 590
 Thr Val Val Glu Gln Ile Ala Asp Lys Glu Thr Gly Glu Phe His Glu
 595 600 605
 Lys Val Thr Leu Gly Glu Ser Val Leu Ala Ala Gly Gln Trp Leu Gln
 610 615 620
 Tyr Gly Val Thr Arg Lys Val Thr Lys Arg Ser Val Met Thr Leu Ala
 625 630 635 640

Tyr Gly Ser Lys Glu Ser Leu Val Arg Gln Gln Val Leu Glu Asp Thr
 645 650 655
 Ile Gln Pro Ala Ile Asp Asn Gly Glu Phe Thr His Gln Pro Asn Gln
 660 665 670
 Ala Ala Gly Tyr Met Ala Lys Leu Ile Asp Ala Ser Thr Ser Val Thr
 675 680 685
 Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys Ser Ala Ala Lys
 690 695 700
 Leu Leu Ala Ala Glu Val Lys Asp Lys Lys Lys Gly Val Ile Leu His
 705 710 715 720
 Arg Cys Ala Val His Trp Val Thr Pro Asp Gly Phe Pro Val Trp Gln
 725 730 735
 Glu Gln Asn Gln Ala Arg Leu Lys Leu Val Phe Leu Gly Gln Ala Asn
 740 745 750
 Val Lys Met Thr Tyr Asn Thr Gly Lys Asp Ser Glu Ile Asp Ala His
 755 760 765
 Lys Gln Glu Ser Gly Ile Ala Pro Asn Phe Val His Ser Gln Asp Gly
 770 775 780
 Ser His Leu Arg Met Thr Val Val His Ala Asn Glu Val Tyr Gly Ile
 785 790 795 800
 Asp Ser Phe Ala Leu Ile His Asp Ser Phe Gly Thr Ile Pro Gly Asn
 805 810 815
 Leu Phe Lys Ala Val Arg Glu Thr Met Val Lys Thr Tyr Glu Asp Asn
 820 825 830
 Asp Val Ile Ala Asp Phe Tyr Asp Gln Phe Ala Asp Gln Leu His Glu
 835 840 845
 Ser Gln Leu Asp Lys Met Pro Ala Val Pro Ala Lys Gly Asp Leu Asn
 850 855 860
 Leu Arg Asp Ile Leu Glu Ser Asp Phe Ala Phe Ala
 865 870 875

<210> 6
 <211> 841
 <212> PRT
 <213> Bacteriophage SP6

<400> 6
 Met Gln Asp Leu His Ala Ile Gln Leu Gln Leu Glu Glu Glu Met Phe
 1 5 10 15
 Asn Gly Gly Ile Arg Arg Phe Glu Ala Asp Gln Gln Arg Gln Ile Ala
 20 25 30
 Ala Gly Ser Glu Ser Asp Thr Ala Trp Asn Arg Arg Leu Leu Ser Glu

35					40					45					
Pro	Met	Ala	Glu	Gly	Ile	Gln	Ala	Tyr	Lys	Glu	Glu	Tyr	Glu	Gly	Lys
50						55					60				
Lys	Gly	Arg	Ala	Pro	Arg	Ala	Leu	Ala	Phe	Leu	Gln	Cys	Val	Glu	Asn
65					70					75					80
Glu	Val	Ala	Ala	Tyr	Ile	Thr	Met	Lys	Val	Val	Met	Asp	Met	Leu	Asn
				85					90					95	
Thr	Asp	Ala	Thr	Leu	Gln	Ser	Val	Ala	Glu	Arg	Ile	Glu	Asp	Gln	Val
			100					105					110		
Arg	Phe	Ser	Lys	Leu	Glu	Gly	His	Ala	Ala	Lys	Tyr	Phe	Glu	Lys	Val
		115					120					125			
Lys	Lys	Ser	Leu	Lys	Ala	Ser	Arg	Thr	Lys	Ser	Tyr	Arg	His	Ala	His
	130					135					140				
Asn	Val	Ala	Val	Val	Ala	Glu	Lys	Ser	Val	Ala	Glu	Lys	Asp	Ala	Asp
145						150					155				160
Phe	Asp	Arg	Trp	Glu	Ala	Trp	Pro	Lys	Glu	Thr	Gln	Leu	Gln	Ile	Gly
				165					170					175	
Thr	Thr	Ile	Leu	Glu	Gly	Ser	Val	Phe	Tyr	Asn	Gly	Glu	Pro	Val	Phe
			180					185					190		
Met	Arg	Ala	Met	Arg	Thr	Tyr	Gly	Gly	Lys	Thr	Ile	Tyr	Tyr	Leu	Gln
		195					200					205			
Thr	Ser	Glu	Ser	Val	Gly	Gln	Trp	Ile	Ser	Ala	Phe	Lys	Glu	His	Val
	210					215					220				
Ala	Gln	Leu	Ser	Pro	Ala	Tyr	Ala	Pro	Cys	Val	Ile	Pro	Pro	Arg	Pro
225						230					235				240
Trp	Arg	Thr	Pro	Phe	Asn	Gly	Gly	Phe	His	Thr	Glu	Lys	Val	Ile	Arg
				245					250					255	
Leu	Val	Lys	Gly	Asn	Arg	Glu	His	Val	Arg	Lys	Leu	Thr	Gln	Lys	Gln
			260					265					270		
Met	Pro	Lys	Val	Tyr	Lys	Ala	Ile	Asn	Ala	Leu	Gln	Asn	Thr	Gln	Trp
		275					280					285			
Gln	Ile	Asn	Lys	Asp	Val	Leu	Ala	Val	Ile	Glu	Glu	Val	Ile	Arg	Leu
	290					295					300				
Asp	Leu	Gly	Tyr	Gly	Val	Pro	Ser	Phe	Lys	Pro	Leu	Ile	Asp	Lys	Glu
305						310					315				320
Asn	Lys	Pro	Ala	Asn	Pro	Val	Pro	Val	Glu	Leu	Arg	Gly	Arg	Glu	Leu
				325					330					335	
Lys	Glu	Met	Leu	Ser	Pro	Glu	Gln	Trp	Gln	Gln	Phe	Ile	Asn	Trp	Lys
			340					345					350		

Gly Glu Cys Ala Arg Leu Tyr Thr Ala Glu Thr Lys Arg Gly Ser Lys
 355 360 365
 Ser Ala Ala Val Val Arg Met Val Gly Gln Ala Arg Lys Tyr Ser Ala
 370 375 380
 Phe Glu Ser Ile Tyr Phe Val Tyr Ala Met Asp Ser Arg Ser Arg Val
 385 390 395 400
 Tyr Val Gln Ser Ser Thr Leu Ser Asn Asp Leu Gly Lys Ala Leu Leu
 405 410 415
 Arg Phe Thr Glu Gly Arg Pro Val Asn Gly Val Glu Ala Leu Lys Trp
 420 425 430
 Phe Cys Ile Asn Gly Ala Asn Leu Trp Gly Trp Asp Lys Lys Thr Phe
 435 440 445
 Asp Val Arg Val Ser Asn Val Leu Asp Glu Glu Phe Gln Asp Met Cys
 450 455 460
 Arg Asp Ile Ala Ala Asp Pro Leu Thr Phe Thr Gln Trp Ala Lys Ala
 465 470 475 480
 Asp Ala Pro Tyr Ala Trp Cys Phe Glu Tyr Ala Gln Tyr Leu Asp Leu
 485 490 495
 Val Asp Glu Gly Arg Ala Asp Glu Phe Arg Thr His Leu Pro Val His
 500 505 510
 Gln Asp Gly Ser Cys Ser Gly Ile Gln His Tyr Ser Ala Met Leu Arg
 515 520 525
 Asp Glu Val Gly Ala Lys Ala Val Asn Leu Lys Pro Ser Asp Ala Pro
 530 535 540
 Gln Asp Ile Tyr Gly Ala Val Ala Gln Val Val Ile Asn Ala Leu Tyr
 545 550 555 560
 Met Asp Ala Asp Asp Ala Thr Thr Phe Thr Ser Gly Ser Val Thr Leu
 565 570 575
 Ser Gly Thr Glu Leu Arg Ala Met Ala Ser Ala Trp Asp Ser Ile Gly
 580 585 590
 Ile Thr Arg Ser Leu Thr Lys Lys Pro Val Met Thr Leu Pro Tyr Gly
 595 600 605
 Ser Thr Arg Leu Thr Cys Arg Glu Ser Val Ile Asp Tyr Ile Val Asp
 610 615 620
 Leu Glu Glu Lys Glu Ala Gln Lys Glu Gly Arg Thr Ala Asn Lys Val
 625 630 635 640
 His Pro Phe Glu Asp Asp Arg Gln Asp Tyr Leu Thr Pro Gly Ala Ala
 645 650 655
 Tyr Asn Tyr Met Thr Ala Leu Ile Trp Pro Ser Ile Ser Glu Val Val
 660 665 670

Lys Ala Pro Ile Val Ala Met Lys Met Ile Arg Gln Leu Ala Arg Phe
675 680 685

Ala Ala Lys Arg Asn Glu Gly Leu Met Tyr Thr Leu Pro Thr Gly Phe
690 695 700

Ile Leu Glu Gln Lys Thr Glu Met Leu Arg Val Arg Thr Cys Leu Met
705 710 715 720

Gly Asp Ile Lys Met Ser Leu Gln Val Glu Thr Asp Ile Val Asp Glu
725 730 735

Ala Ala Met Met Gly Ala Ala Ala Pro Asn Phe Val His Gly His Asp
740 745 750

Ala Ser His Leu Ile Leu Thr Val Cys Glu Leu Val Asp Lys Gly Val
755 760 765

Thr Ser Ile Ala Val Ile His Asp Ser Phe Gly Thr His Ala Leu Thr
770 775 780

Leu Arg Val Ala Leu Lys Gly Gln Met Val Ala Met Tyr Ile Asp Gly
785 790 795 800

Asn Ala Leu Gln Lys Leu Leu Glu Glu His Glu Val Arg Trp Met Val
805 810 815

Asp Thr Gly Ile Glu Val Pro Glu Gln Gly Glu Phe Asp Leu Asn Glu
820 825 830

Ile Met Asp Ser Glu Tyr Val Phe Ala
835 840

<210> 7
<211> 78
<212> PRT
<213> Bacteriophage T7

<400> 7
Tyr Gly Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala
1 5 10 15

Tyr Gly Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Asp Thr
20 25 30

Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro
35 40 45

Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser
50 55 60

Val Thr Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys
65 70 75

<210> 8
<211> 78
<212> PRT

<213> Bacteriophage T7

<220>

<221> PEPTIDE

<222> (1)..(78)

<223> Mutant T7 RNA polymerase F644Y.

<400> 8

Tyr Gly Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala
1 5 10 15

Tyr Gly Ser Lys Glu Tyr Gly Phe Arg Gln Gln Val Leu Glu Asp Thr
20 25 30

Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro
35 40 45

Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu Thr Trp Glu Ser Val Ser
50 55 60

Val Thr Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys
65 70 75

<210> 9

<211> 78

<212> PRT

<213> Bacteriophage T7

<220>

<221> PEPTIDE

<222> (1)..(78)

<223> Mutant T7 RNA polymerase F646Y.

<400> 9

Tyr Gly Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala
1 5 10 15

Tyr Gly Ser Lys Glu Phe Gly Tyr Arg Gln Gln Val Leu Glu Asp Thr
20 25 30

Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro
35 40 45

Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser
50 55 60

Val Thr Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys
65 70 75

<210> 10

<211> 78

<212> PRT

<213> Bacteriophage T7

<220>

<221> PEPTIDE

<222> (1)..(78)

<223> Mutant T7 RNA polymerase L665P/F667Y.

<400> 10

Tyr Gly Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala
1 5 10 15

Tyr Gly Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Asp Thr
20 25 30

Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly Pro Met Tyr Thr Gln Pro
35 40 45

Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser
50 55 60

Val Thr Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys
65 70 75

<210> 11

<211> 73

<212> PRT

<213> Bacteriophage T7

<400> 11

Ala Gly Gln Trp Leu Ala Tyr Gly Val Thr Arg Ser Val Thr Lys Arg
1 5 10 15

Ser Val Met Thr Leu Ala Tyr Gly Ser Lys Glu Phe Gly Phe Arg Gln
20 25 30

Gln Val Leu Glu Asp Thr Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly
35 40 45

Leu Met Phe Thr Gln Pro Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu
50 55 60

Ile Trp Glu Ser Val Ser Val Thr Val
65 70

<210> 12

<211> 73

<212> PRT

<213> Bacteriophage T7

<220>

<221> PEPTIDE

<222> (1)..(73)

<223> Mutant T7 RNA polymerase F644Y.

<400> 12

Ala Gly Gln Trp Leu Ala Tyr Gly Val Thr Arg Ser Val Thr Lys Arg
1 5 10 15

Ser Val Met Thr Leu Ala Tyr Gly Ser Lys Glu Tyr Gly Phe Arg Gln
20 25 30

Gln Val Leu Glu Asp Thr Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly

35 40 45
 Leu Met Phe Thr Gln Pro Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu
 50 55 60

Ile Trp Glu Ser Val Ser Val Thr Val
 65 70

<210> 13
 <211> 73
 <212> PRT
 <213> Bacteriophage T7

<220>
 <221> PEPTIDE
 <222> (1)..(73)
 <223> Mutant T7 RNA polymerase L665P/F667Y.

<400> 13
 Ala Gly Gln Trp Leu Ala Tyr Gly Val Thr Arg Ser Val Thr Lys Arg
 1 5 10 15

Ser Val Met Thr Leu Ala Tyr Gly Ser Lys Glu Phe Gly Phe Arg Gln
 20 25 30

Gln Val Leu Glu Asp Thr Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly
 35 40 45

Pro Met Tyr Thr Gln Pro Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu
 50 55 60

Ile Trp Glu Ser Val Ser Val Thr Val
 65 70

<210> 14
 <211> 73
 <212> PRT
 <213> Bacteriophage T3

<400> 14
 Ala Gln Gln Trp Leu Ala Tyr Gly Val Thr Arg Ser Val Thr Lys Arg
 1 5 10 15

Ser Val Met Thr Leu Ala Tyr Gly Ser Lys Glu Phe Gly Phe Arg Gln
 20 25 30

Gln Val Leu Asp Asp Thr Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly
 35 40 45

Leu Met Phe Thr Gln Pro Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu
 50 55 60

Ile Trp Asp Ala Val Ser Val Thr Val
 65 70

<210> 15
 <211> 73

<212> PRT
 <213> Bacteriophage K11

<400> 15
 Ala Ala Gln Trp Leu Gln Tyr Gly Val Thr Arg Lys Val Thr Lys Arg
 1 5 10 15
 Ser Val Met Thr Leu Ala Tyr Gly Ser Lys Glu Ser Leu Val Arg Gln
 20 25 30
 Gln Val Leu Glu Asp Thr Ile Gln Pro Ala Ile Asp Asn Gly Glu Gly
 35 40 45
 Leu Met Phe Thr His Pro Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu
 50 55 60
 Ile Trp Asp Ala Val Thr Val Thr Val
 65 70

<210> 16
 <211> 75
 <212> PRT <
 213> Bacteriophage SP6

<400> 16
 Ala Ser Ala Trp Asp Ser Ile Gly Ile Thr Arg Ser Leu Thr Lys Lys
 1 5 10 15
 Pro Val Met Thr Leu Pro Tyr Gly Ser Thr Arg Leu Thr Cys Arg Glu
 20 25 30
 Ser Val Ile Asp Tyr Ile Val Asp Leu Glu Glu Lys Glu Ala Gln Lys
 35 40 45
 Ala Val Ala Glu Gly Arg Thr Ala Asn Lys Val His Pro Phe Glu Asp
 50 55 60
 Asp Arg Gln Asp Tyr Leu Thr Pro Gly Ala Ala
 65 70 75

<210> 17
 <211> 31
 <212> DNA
 <213> Bacteriophage T7

<220>
 <221> misc_feature
 <222> (1)..(31)
 <223> Mutant T7 RNA polymerase wild type.

<220>
 <221> misc_feature
 <222> (25)..(25)
 <223> Nucleotide 25 is "n" wherein "n" = any nucleotide.

<400> 17
 gggagggggg ggggggggcc cccnngggcg t

31

<210> 18
 <211> 32
 <212> DNA
 <213> Bacteriophage T7

<220>
 <221> misc_feature
 <222> (1)..(32)
 <223> Mutant T7 RNA polymerase wild type.

<220>
 <221> misc_feature
 <222> (1)..(32)
 <223> Nucleotides 6-8, 18, 25-30 are "n" wherein "n" = any nucleotide.

<400> 18
 gcgtcnnaa aacgcacntt ttctntogtn gg 32

<210> 19
 <211> 19
 <212> DNA
 <213> Bacteriophage T7

<220>
 <221> misc_feature
 <222> (1)..(19)
 <223> Mutant T7 RNA polymerase F644Y.

<400> 19
 cgaggggggg ccggtaccc 19

<210> 20
 <211> 25
 <212> DNA
 <213> Bacteriophage T7

<220>
 <221> misc_feature
 <222> (1)..(25)
 <223> Mutant T7 RNA polymerase F644Y.

<220>
 <221> misc_feature
 <222> (6)..(6)
 <223> Nucleotide 6 is "n" wherein "n" = any nucleotide.

<400> 20
 cccctntttg ttcttttagt gaggt 25

<210> 21
 <211> 18
 <212> DNA
 <213> Bacteriophage T7

```

<220>
<221> misc_feature
<222> (1)..(18)
<223> Mutant T7 RNA polymerase F667Y.

<400> 21
gagggggggcc ggtaacgc 18

<210> 22
<211> 22
<212> DNA
<213> Bacteriophage T7

<220>
<221> misc_feature
<222> (1)..(22)
<223> Mutant T7 RNA polymerase F667Y.

<400> 22
acgccttttg ttcccttttag tg 22

<210> 23
<211> 569
<212> DNA
<213> Bacteriophage T7
<220>
<221> misc_feature
<222> (1)..(569)
<223> Mutant T7 RNA polymerase F644Y/L665P/F667Y.

<220>
<221> misc_feature
<222> (1)..(472)
<223> Nucleotides 1-14, 17-18, 21, 26, 29, 34, 38, 40, 50-51, 53, 58, 7
5-76, 85, 110, 117, 132, 142, 150, 157, 399, 440 and 472 are "n"
wherein "n" = any nucleotide

<400> 23
nnnnnnnnnn nnnnggnggt nggttncgna tccnaaangn aacaggggggn nantgtgnaa 60
acatgaatat ttttnntaag ctttnattcc agggcaagac attttaaccn aaattgncaa 120
attatatcac tnattagaca gnaaaatctn acccagntaa gacttctgga ggtttggtac 180
agtagtttgt cttggatgct tcatgtatgc agtcacttat agtcagtatt gcacttggca 240
cacttcagct taaaccaaca ggataggaaa aatagggagc aacatggagt ggcatcctgg 300
tatttctaca gtccgttaga tgaagtctct atatgtgcaa catcctggga cagagcatat 360
ttgggaagaa acagtttgcc attgaatccc gtgtcatana atatccagca cagatggtgg 420
tgttgatggt tagcaataan cacactctct cttttcgatg tgcaattgtat antcaggtgg 480
atacaaaaag acatcgcttg gccacatgc aaggccaaaa agcagacatc agaaagagag 540
cagtcatgtg ggggaattgg tccgactgc 569

```

<210> 24
 <211> 50
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> T7Rpol-N primer

 <400> 24
 atatttttagc catggaggat tgatatatga acacgattaa catcgctaag 50

 <210> 25
 <211> 40
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> T7Rpol-C primer

 <400> 25
 atatttttagc catggtatag tgagtcgtat tgatttggcg 40

 <210> 26
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> F646Y(+) primer

 <400> 26
 gttgacggaa gccgtactct ttggac 26

 <210> 27
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> F646Y(-) primer

 <400> 27
 gtccaaagag tacggcttcc gtcaac 26

 <210> 28
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> T7RNAP-HpaI-N primer

 <400> 28
 cgcgcggtta acttgcttcc tag 23

 <210> 29
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pTrc99a-PstI-C primer

 <400> 29
 gcatgcctgc aggtcgactc tag 23

 <210> 30
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> ApaF1 primer

 <400> 30
 catctggtcg cattgggtca c 21

 <210> 31
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Xho-R primer

 <400> 31
 ccaagtgttc tcgagtggag a 21

 <210> 32
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Xho-F primer

 <400> 32
 ctaagtctcc actcgagaac acttgg 26

 <210> 33
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> AflIII-R primer

 <400> 33
 cagccagcag cttagcagca g 21

 <210> 34
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> 667R primer

 <400> 34

Cont
Fl
gctgagtgtgta catcggaccc t

21

<210> 35
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> 667F primer

<400> 35
gctgagtgtgta catcggaccc t

21

<210> 36
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> T7-DOUBLE-R primer

<400> 36
ctctttggac ccgtaagcca g

21

<210> 37
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> T7-DOUBLE-F primer

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29

<210> 38
<211> 19
<212> DNA
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<223> L220 primer

<400> 38
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19

<210> 39
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
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22